

SEQUENCE LISTING

- (1) GENERAL NFORMATION:
 - (i) APPLICANT:

Bazin, Hervé

Latinne, Dominique

Kaplan, Ruth

Kieber-Emmons, Thomas

Postema, Christina E.

White-Scharf, Mary

(ii) TITLE OF INVENTION: LO-CD2a Antibody and Uses

> Thereof for Inhibiting

> T-Cell Activation and

Proliferation

- (iii) NUMBER OF SEQUENCES:
- CORRESPONDENCE ADDRESS: (iv)
 - ADDRESSEE: (A)

Carella, Byrne, Bain, Gilfillan,

Cecchi, Stewart & Olstein

- (B) STREET: 6 Becker Farm Road
- CITY: Roseland (C)
- STATE: New Jersey (D)
- (E) COUNTRY: | U.S.A.
- ZIP: 07d68 (F)
- COMPUTER READABLE FORM: (v)
 - MEDIUM TYPE: 3.5 inch diskette (A)
 - (B) COMPUTER: IBM PS/2
 - OPERATING SYSTEM: MS-DOS (C)

- (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/477,989
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/407,009
 - (B) FILING DATE: 29-MAR-1995
 - (A) APPLICATION NUMBER: 08/119,032
 - (B) FILING DATE: 09-SEP-1993
 - (A) APPLICATION NUMBER: 08/027,008
 - (B) FILING DATE: 05-MAR-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Olstein, Elliot M.
 - (B) REGISTRATION NUMBER: 24,025
 - (C) REFERENCE/DOCKET NUMBER: 61750-147
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: oligonucleotide
 - (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AACCCGGGGA CATTCAGCTG ACCCAGTCTC AA

32

- (2) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGTCGACTA CAGTTGGTGC AGCATCAGC

- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACCCGGGGA GGTCCAGCTG CAGCAGTCTG G

31

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGTCGACCC AGTGGATAGA CCGATGG

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGCAAGCTT CATGGGATGG AG

- (2) INFORMATION FOR SEQ ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: GCTGCTTGGG GACTGGGTCA GCTGGAT

- (2) INFORMATION FOR SEQ ID NO: 7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATTCAGCTGA CCCAGTCTCC A

21

- (2) INFORMATION FOR SEQ ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

 GATCGGATCC ACCTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTCAGT TCCAGCTT

- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCTCCTGCAG TGGGACCTCG GAGTGGACAC C

31

- (2) INFORMATION FOR SEQ ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTCCAGC TGCAGCAGTC T

- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGATGTATCA GCTGTCAGTG TGGC

24 ·

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCCACACTGA CAGCTGATAC ATCG

- (2) INFORMATION FOR SEQ ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAGAGTGCCT TGGCCCCAGT A

21

- (2) INFORMATION FOR SEQ ID NO: 14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TACTGGGGCC AAGGCACCCT CGTCACA

- (2) INFORMATION FOR SEQ ID NO: 15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCGGATCC CTATAAATCT CTGGC

25

- (2) INFORMATION FOR SEQ ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGGATCCGC GGCCGCGTCG ACTACAGTTG GTGCAGCATC AGC

- (2) INFORMATION FOR SEQ ID NO: 17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGGATCCGC GGCCGCGTCG ACCCAGTGGA TAGACCGATG G

41

- (2) INFORMATION FOR SEQ ID NO: 18:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCATGGCCTC GAGGGCCCCC CCCCCCCCC C

- (2) INFORMATION FOR SEQ ID NO: 19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCTGTTTAGG CCTCTGCTTC ACCCAGTAC

29

- (2) INFORMATION FOR SEQ ID NO: 20:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGATAATGGG TAAATTGCAT GCAGTAATA

- (2) INFORMATION FOR SEQ ID NO: 21:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGCAAGCTTC ATGATGAGTC CTGTCCAGTC

30

- (2) INFORMATION FOR SEQ ID NO: 22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AGTAAGCTTC ATGAAATGCA GGTGGATC

- (2) INFORMATION FOR SEQ ID NO: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGGAGATTGC TGCAGCTGGA CTTC

24

- (2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 - (2) INFORMATION FOR SEQ ID NO: 25:

		(A) LENGTH: 61 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	•		
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
,	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
AGAATGGCCA CO	GTCAT	CCGA CCCCCTCAGA GTTTACTATT CTACTATCCA ACTGAGGAAG	60
С		·	61
	(2)	INFORMATION FOR SEQ ID NO: 26:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 34 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
GATCGAATTC GO	CCACCA	ATGA AATGCAGGTG GATC	34

SEQUENCE CHARACTERISTICS:

(i)

- (2) INFORMATION FOR SEQ ID NO: 27:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
 - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCAGAAAGCT AGCTTGCCAT CCCTATAAAT CTCTGGC

37

- (2) INFORMATION FOR SEQ ID NO: 28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Val Val Leu Thr Gln Thr Pro Pro Thr

5

10

Leu Leu Ala Thr Ile Gly Gln Ser Val Ser

15 20

Ile Ser Cys

- (2) INFORMATION FOR SEQ ID NO: 29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Val Val Met Thr Gln Ser Pro Leu Ser

5

10

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser

15 20

Ile Ser Cys

- (2) INFORMATION FOR SEQ ID NO: 30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Trp Leu Leu Gln Arg Thr Gly Gln Ser Pro

5

10

Gln Pro Leu Ile Tyr

(2)	INFORMATION	FOR	SEO	ID	NO:	31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro

5

10

Arg Arg Leu Ile Tyr

15

- (2) INFORMATION FOR SEQ ID NO: 32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gly Val Pro Asn Arg Phe Ser Gly Ser Gly

5

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser

15 20

Gly Val Glu Ala Glu Asp Leu Gly Val Tyr

25 30

Tyr Cys

- (2) INFORMATION FOR SEQ ID NO: 33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

5

10

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser

15 20

Arg Val Glu Ala Glu Asp Val Gly Val Tyr

25 30

Tyr Cys

- (2) INFORMATION FOR SEQ ID NO: 34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

5

10

- (2) INFORMATION FOR SEQ ID NO: 35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

5

- (2) INFORMATION FOR SEQ ID NO: 36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
GCAAGAGATG (GAAGCT	GGTT GTCCCAAGGT TACCAATAAT GAAGGTGGAC TCTGGGTCAT	60
CACAACATCA	CCATTG	GTTC C	81
(2)	INFO	RMATION FOR SEQ ID NO: 37:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 37:	
CAACCAGCTT (CCATCT	CTTG CAGGTCAAGT CAGAGTCTCT TACATAGTAG TGGAAACACC	60
TATTTAATT G	G		72
		77	
(2)	INFO	RMATION FOR SEQ ID NO: 38:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 81 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: oligonucleotide

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
AGATTCCAGT	TTGGAT	ACCA AATAAATTAG CGGCTGTGGA GATTGGCCTG GCCTTAGCAA	60
CCAATTTAAA	TAGGTG	TTTC C	81
(2)	INFO	RMATION FOR SEQ ID NO: 39:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 81 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 39:	
TTGGTATCCA	AACTGG	AATC TGGGGTCCCC GACAGGTTCA GTGGCTCAGG GAGTGGAACA	60
GATTTCACAC	TCAAAA'	TCAG T	81
(2)	INFO	RMATION FOR SEQ ID NO: 40:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: oligonucleotide

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
ATGGGTAAAT	TGCATG	CAGT AATAAACCCC CACATCCTCA GCTTCCACTC CACTGATTTT	60
GAGTGTGAAA	TC		72
(2)	INFO	RMATION FOR SEQ ID NO: 41:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 63 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 41:	
TACTGCÀTGC	AATTTA(CCCA TTATCCGTAC ACGTTTGGAC AAGGGACCAA GCTGGAAATC	60
AAA			63
(2)	INFO	RMATION FOR SEQ ID NO: 42:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 67 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: oligonucleotide

(ii	.) MOLECULE TYPE: oligonucleotide	
(ix) FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi	.) SEQUENCE DESCRIPTION: SEQ ID NO: 42:	
GATCGGATCC AACTC	GAGGAA GCAAAGTTTA AATTCTACTC ACGTTTGATT TCCAGCTTGG	60
TCCCTTG		67
(2) INF	ORMATION FOR SEQ ID NO: 43:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: oligonucleotide	
(ix) FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
GATCAAGCTT CATG	ATGAGT CCT	23
(2) INF	ORMATION FOR SEQ ID NO: 44:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 21 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: oligonucleotide	

		(A) NAME/KEY: PCR primer
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 44:
GCAAGAGATG	GAAGCT	GGTT G
(2)	INFO	RMATION FOR SEQ ID NO: 45:
	(i)	SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 21 bases
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: single
		(D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: oligonucleotide
	(ix)	FEATURE:
		(A) NAME/KEY: PCR primer
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 45:
CAACCAGCTT	CCATCT	CTTG C
(2)	INFO	RMATION FOR SEQ ID NO: 46:
	(i)	SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 21 bases

21 .

21

(ix) FEATURE:

(A) NAME/KEY: PCR primer

(B)

(C)

(D)

(ix) FEATURE:

TYPE: nucleic acid

TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

STRANDEDNESS: single

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
AGATTCCAGT	TTGGAT	ACCA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 47:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 47:	
TTGGTATCCA	AACTGG	AATC TGGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 48:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
ATGGGTAAAT	TGCATG	CAGT AATA	24

(2)	INFO	RMATION FOR SEQ ID NO: 49:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
TACTGCATGC	AATTTA	CCCA TTAT	24
(2)	INFO	RMATION FOR SEQ ID NO: 50:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 26 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
GATCGGATCC A	AACTGA	GGAA GCAAAG	26
(2)		RMATION FOR SEQ ID NO: 51:	
	(i)	SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu

5

Leu Gln Arg Pro Gly Ala Ser Val Lys Leu

15 20

Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr

25 30

- (2) INFORMATION FOR SEQ ID NO: 52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

5

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
25 30

- (2) INFORMATION FOR SEQ ID NO: 53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Trp Val Lys Gln Arg Pro Lys Gln Gly Leu

10

Glu Leu Val Gly

- (2) INFORMATION FOR SEQ ID NO: 54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

5

Glu Trp Met Gly

- (2) INFORMATION FOR SEQ ID NO: 55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser

5

10

Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu

15 20

Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys

25 30

Ala Arg

- (2) INFORMATION FOR SEQ ID NO: 56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56: Arg Val Thr Met Thr Arg Asp Thr Ser Ile 5 10 Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu

15 20

Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

25 30

Ala Arg

- (2) INFORMATION FOR SEQ ID NO: 57:
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 11 amino acids
 - TYPE: amino acid (B)
 - (C) STRANDEDNESS:
 - TOPOLOGY: (D) linear
 - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Trp Gly Gln Gly Thr Leu Val Thr Val Ser

10 5

Ser

- INFORMATION FOR SEQ ID NO: 58: (2)
 - (i) SEQUENCE CHARACTERISTICS:
 - LENGTH: 11 amino acids (A)
 - amino acid TYPE: (B)

(D) TOPOLOGY: Tinear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
5 10
Ser
(2) INFORMATION FOR SEQ ID NO: 59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURE:
(A) NAME/KEY: PCR primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
GATCAAGCTT CATGAAATGC AGGTGGATCA TCCTCTTCTT GATGGCAGTA GCTACAGGTA 60
AGGCACTCCC AAGTCGTAAA CTTGAGA 88
(2) INFORMATION FOR SEQ ID NO: 60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(C)

STRANDEDNESS:

		(D) T	COPOLOGY:	linear	
	(ii)	MOLECU	LE TYPE:	oligonucleotide	
	(ix)	FEATUR	RE:		
		(A) N	JAME/KEY:	PCR primer	
÷	(xi)	SEQUEN	ICE DESCRII	PTION: SEQ ID NO: 60:	
CACCTGTGAG TT	rgaccc	CTG TTG	AAAGAAA TCCA	AAAGATA GTGTCACTGT CTCCCAAGTG	60
TATGATCTCT CA	AGTTI	AGG ACT	TGGG		87
(2)	INFOR	MATION	FOR SEQ	ID NO: 61:	÷
((i)	SEQUEN	ICE CHARACT	TERISTICS:	
		(A) L	ENGTH: 78	bases	
		(B) I	YPE: nucl	leic acid	
		(C) S	TRANDEDNES	SS: single	
		(D) T	OPOLOGY:	linear	
((ii)	MOLECU	LE TYPE:	oligonucleotide	
((ix)	FEATUR	E:		
		(A) N	AME/KEY:	PCR primer	
((xi)	SEQUEN	CE DESCRIE	PTION: SEQ ID NO: 61:	
ACAGGGGTCA AC	TCACA	GGT GCA	GCTGGTG CAGT	CTGGGG CTGAGGTGAA GAAGCCTGGG	60
GCCTCAGTGA AG	GTCTC	С			78
(2)	NFOR	MATION	FOR SEQ I	ID NO: 62:	
((i)	SEQUEN	CE CHARACT	TERISTICS:	
		(A) L	ENGTH: 78	bases	
		(B) T	YPE: nucl	leic acid	
		(C) S	TRANDEDNES	SS: single	

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 62:	
GGCCTGTCGC	ACCCAG	TACA TATAGTACTC GGTGAAGGTG TATCCAGAAG CCTTGCAGGA	60
GACCTTCACT	GAGGCC	cc	78
(2)	INFO	RMATION FOR SEQ ID NO: 63:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 78 bases	
		(B) TYPE: nucleic acid	
	•	(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 63:	
ATGTACTGGG	TGCGAC	AGGC CCCTGGACAA GGGCTTGAGC TGATGGGAAG GATCGATCCT	60 .
GAAGACGGTA	GTATTG	AT	78
(2)	INFO	RMATION FOR SEQ ID NO: 64:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 78 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 64:	
TGTGCTAGAG	GACGTG	TCAG CGGTCAGGGT GACCTTTTTC TTAAACTTCT CAACATAATC	60
AATACTACCG	TCTTCA	GG .	78
		•	
(2)	INFO	RMATION FOR SEQ ID NO: 65:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 84 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
	•	(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 65:	
GCTGACACGT	CCTCTA	GCAC AGCCTACATG GAGCTGAGCA GCCTGACCTC TGACGACACG	60
GCCGTGTATT	ACTGTG	CGAG AGGA	84
(2)	INFO	RMATION FOR SEQ ID NO: 66:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 87 bases	
		(B) TYPE: nucleic acid	
<u>.</u>		(C) STRANDEDNESS: single	

TOPOLOGY:

(D)

linear

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 66:	
GGACTCACCT G	AGGAGA	ACGG TGACCAGGGT TCCTTGGCCC CAGTAAGCAA ACCTATAGTT	60
AAACTTTCCT C	rcgcac	CAGT AATACAC	87
(2')	INFOR	MATION FOR SEQ ID NO: 67:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 69 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
,		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 67:	
ACCGTCTCCT CA	AGGTGA	GTC CTTACAACCT CTCTCTTCTA TTCAGCTTAA ATAGATTTTA	60
CTGCATTTG			69
(2)	INFOR	MATION FOR SEQ ID NO: 68:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 69 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

	(ii)	MOLECULE TYPE: oligonucleotide	
		FEATURE:	
	(IX)		
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 68:	
CCTAGTCCTT	CATGAC	CTGA AATTCAGATA CACACATTTC CCCCCCAACA AATGCAGTAA	60
AATCTATTT			69
(2)	INFO	RMATION FOR SEQ ID NO: 69:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 69:	
TTCAGGTCAT	GAAGGA	CTAG GGACACCTTG GGAGTCAGAA AGGGTCATTG GGAGCCCGGG	60
CTGATGCAGA	CA		72
(2)	INFO	RMATION FOR SEQ ID NO: 70:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 70:	
GATCGGATCC CT	TATAA	ATCT CTGGCCATGA AGTCTGGGAG CTGAGGATGT CTGTCTGCAT	60
CAGCCCGGGC TO	2		72
(2)	INFOR	RMATION FOR SEQ ID NO: 71:	
ı	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 25 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
((ii)	MOLECULE TYPE: oligonucleotide	
((ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
((xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 71:	
GATCAAGCTT CA	TGAAA	ATGC AGGTG	25
(2)	NFOR	MATION FOR SEQ ID NO: 72:	
. ((i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 72:	
CACCTGTGAG	TTGACC	CCTG TTG	23
(2)	INFO	RMATION FOR SEQ ID NO: 73:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 73:	
ACAGGGGTCA	ACTCAC.	AGGT G	21
(2)	INFO	RMATION FOR SEQ ID NO: 74:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		· · · · · · · · · · · · · · · · · · ·	

(ii) MOLECULE TYPE: oligonucleotide

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 74:	
GGCCTGTCGC .	ACCCAG	TACA T	21
(2)	INFO	RMATION FOR SEQ ID NO: 75:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
	•	(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 75:	
ATGTACTGGG	rgcgac	AGGC C	21
(2)	INFO	RMATION FOR SEQ ID NO: 76:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 76:	

(A) NAME/KEY: PCR primer

TGTGCTAGAG	GACGTGTCAG C	21

(2)	INFORMATION FOR SEQ ID NO: //:							
	(i)	SEQUENCE CHARACTERISTICS:						
		(A) LENGTH: 21 bases						
		(B) TYPE: nucleic acid						
		(C) STRANDEDNESS: single						
		(D) TOPOLOGY: linear						
	(ii)	MOLECULE TYPE: oligonucleotide						
	(ix)	FEATURE:						
		(A) NAME/KEY: PCR primer						
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 77:						
GCTGACACGT (CCTCTA	GCAC A	21					
(2)	INFO	RMATION FOR SEQ ID NO: 78:						
	(i)	SEQUENCE CHARACTERISTICS:						
		(A) LENGTH: 21 bases						
		(B) TYPE: nucleic acid						
		(C) STRANDEDNESS: single						
		(D) TOPOLOGY: linear						
	(ii)	MOLECULE TYPE: oligonucleotide						
	(ix)	FEATURE:						
		(A) NAME/KEY: PCR primer						
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 78:						
GGACTCACCT C	SAGGAG	ACGG T	21					

(2)	INFO	RMATION FOR SEQ ID NO: 79:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 79:	
ACCGTCTCCT	CAGGTG	AGTC C	21
(2)	INFO	RMATION FOR SEQ ID NO: 80:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 80:	
CCTAGTCCTT	CATGAC	CTGA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 81:	
	(i)	SEQUENCE CHARACTERISTICS:	

		(A) LENGTH: 21 bases
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: single
		(D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: oligonucleotide
	(ix)	FEATURE:
		(A) NAME/KEY: PCR primer
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 81:
TTCAGGTCAT G	SAACGA	ACTAG G 21
(2)	INFO	RMATION FOR SEQ ID NO: 82:
	(i)	SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 26 bases
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: single
		(D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: oligonucleotide
	(ix)	FEATURE:
		(A) NAME/KEY: PCR primer
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 82:
GATCGGATCC C	TATAA	ATCT CTGGCC 26
(2)	INFO	RMATION FOR SEQ ID NO: 83:
	(i)	SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 761 bases
		(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
- (A) NAME/KEY: Nucleotide sequence encoding LO-CD2a $\ensuremath{V_L}$ chain.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ATGATGAGTC CTG	CCAGTC CCTGTTTCTC	TTATTGCTTT	GGATTCTGGG	TAAGTAGAGA	60
ATGAGTTACA GGAG	CAAGAAT GGGGATGGAG	GATGAGTTCT	GACTGCCCAT	GTTGGCTGTC	120
CATGTGTGGT AAG	GCAGGTC CTATTTCT	AGATGGACAC	TTGAGATTCC	ATTACTTGAT	180
AATGAGAAAT TACA	AGATGAG ATAGGATTTG	TGCTAAGAGG	ATTCTAATGT	AGATGAGAAG	240
GTGTATGCCA TTT	AGGATCT GCAACCGAAT	TGTTTTGTGA	AAAAGCATTT	GGTATATTTT	300
TTAAAAATCA CAAA	AACACAC CGGGATCTCA	CAGGAAATGA	GTAACAAAAA	GTAATTCACA	360
AAGATTGGTT GCAA	AATTTTG CACATAACTT	TGTTCTGATC	TATTATAATT	TCAGGAACCA	420
ATGGTGATGT TGTG	GCTGACC CAGACTCCAC	CTACTTTATT	GGCTACCATT	GGACAATCAG	480
TCTCCATCTC TTGC	CAGGTCA AGTCAGAGTC	TCTTACATAG	TAGTGGAAAC	ACCTATTTAA	540
ATTGGTTGCT ACAG	GAGGACA GGCCAATCTC	CACAGCCGCT	AATTTATTTG	GTATCCAAAC	600
TGGAATCTGG GGTC	CCCCAAC AGGTTCAGTG	GCAGTGGGTC	AGGAACAGAT	TTCACACTCA	660
AAATCAGTGG AGTG	GGAAGCT GAGGATTTGG	GGGTTTATTA	CTGCATGCAA	TTTACCCATT	720
ATCCGTACAC GTTT	rggagct gggaccaago	TGGAACTGAA	A		761

- (2) INFORMATION FOR SEQ ID NO: 84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

(A) NAME/KEY: Chimeric LO-CD2a V_L Chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Met Met Ser Pro Val Gln Ser Leu Phe

-20 -15

Leu Leu Leu Trp Ile Leu Gly Thr Asn

-10 -5

Gly Asp Val Val Leu Thr Gln Thr Pro

-1 +1 5

Pro Thr Leu Leu Ala Thr Ile Gly Gln Ser

10 15

Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

20 25

Leu His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

30 35 40

Leu Leu Gln Arg Thr Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Leu Gly Val

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu

105 110

Leu Lys

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
- (A) NAME/KEY: Nucleotide sequence encoding LO-CD2a $\ensuremath{V_{H}}$ chain.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

ATGAAATGCA	GGTGGATCAT	CCTCTTCTTG	ATGGCAGTAG	CTACAGGTAA	GGCACTCCCA	60
AGTCCTAAAC	TTGAGAGATC	ATACACTTGG	GAGACAGTGA	CACTATCTTT	GGATTTCTTT	120
CAACAGGGGT	CAACTCAGAA	GTCCAGCTGC	AGCAATCTGG	GCCTGAGCTT	CAGAGACCCG	180
GGGCCTCAGT	CAAGTTGTCG	TGCAAGGCTT	CTGGCTATAT	ATTTACAGAA	TACTATATGT	240
ACTGGGTGAA	GCAGAGGCCT	AAACAGGGCC	TGGAATTAGT	AGGAAGGATC	GATCCTGAAG	300
ACGGTAGTAT	TGATTATGTT	GAGAAGTTCA	AAAAGAAGGC	CACACTGACT	GCAGATACAT	360
CGTCCAACAC	AGCCTACATG	CAACTCAGCA	GCCTGACATC	TGAGGACACA	GCAACCTATT	420
TTTGTGCTAG	GGGAAAATTC	AACTATCGAT	TTGCTTACTG	GGGCCAAGGC	ACCCTCGTCA	480
CAGTCTCCTC	Α					491

(2)	INFORM	ATION FOR SEQ ID NO: 86:	
	(i) S	EQUENCE CHARACTERISTICS:	
	•	A) LENGTH: 137 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS:	
	(D) TOPOLOGY: linear	
	(ii) M	OLECULE TYPE: polypeptide	
	(ix) F	EATURE:	
	(A) NAME/KEY: Amino acid sequence of chimeric L	- ٥د
CD2a V _H	chain.		
	(xi) S	EQUENCE DESCRIPTION: SEQ ID NO: 86:	
Met Lys	Cys Arg	Trp Ile Ile Leu Phe Leu	
-19		-15 -10	
Met Ala	Val Ala	Thr Gly Val Asn Ser Glu	
		-5 -1 +1	
Val Gln	Leu Gln	Gln Ser Gly Pro Glu	
	5	10	
Leu Gln	Arg Pro	Gly Ala Ser Val Lys Leu	
		15 20	
Ser Cys	Lys Ala	Ser Gly Tyr Ile Phe Thr	
		25 30	
Glu Tyr	Tyr Met	Tyr Trp Val Lys Gln Arg	
-		35 40	

Pro Lys Gln Gly Leu Glu Leu Val Gly Arg

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr 55 60 Val Glu Lys Phe Lys Lys Lys Ala Thr Leu 65 70 Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr 75 80 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp 85 Thr Ala Thr Tyr Phe Cys Ala Arg Gly Lys 95 100 Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln 105 110

(2) INFORMATION FOR SEQ ID NO: 87:

Gly Thr Leu Val Thr Val Ser Ser

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:
 - (A) NAME/KEY: Rat LO-CD2a light chain variable region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Asp Val Val Leu Thr Gln Thr Pro Pro Thr

5 10

Leu Leu Ala Thr Ile Gly Gln Ser Val Ser

15 20

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu

25 30

His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

35 40

🏿 Leu Leu Gln Arg Thr Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Leu Gly Val

85 90

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu

105 110

Leu Lys

	IN	FORI	MATI	ON FO	OR S	EQ I	D NO	: 88:			
	(i	.) :	SEQUI	ENCE	CHAI	RACT	ERIS	rics:			
			(A)	LEN	GTH:	112	amiı	no acids			
			(B)	TYPI	Ξ: a	amin	o ac	id			
			(C)	STRA	ANDEI	DNES	S:				
			(D)	TOPO	oLOG:	Y: :	linea	ar			
	(i	i) N	MOLE	CULE	TYPI	E:]	poly	peptide			
·	(i	x) I	FEAT	JRE:							
			(A)	NAM	E/KE	Υ:	Hur	nanized	LO-CD2a	light	chain
		7	varia	able	reg:	ion.		•			
	(x	i) S	SEQUI	ENCE	DESC	CRIP	rion:	SEQ I	D NO: 88:		
Val	Val	Met	Thr	Gln	Ser	Pro	Pro	Ser			
			5					10			
Leu	Val	Thr	Leu	Gly	Gln	Pro	Ala	Ser			
			15					20			
Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu			
			25					30			
Ser	Ser	Gly	Asn	Thr	Tyr	Leu	Asn	Trp			
			35					40			
Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln			•
			45					50			
Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu			
			55				•	60			
	Leu Ser Ser	(i (i (x Val Val Leu Val Ser Cys Ser Ser	(ii) (ix) (ix) (xi) (xi) (xi) (xi) (xi)	(i) SEQUION (A) (A) (B) (C) (D) (ii) MOLEC (ix) FEATT (A) variat (xi) SEQUION Val Val Met Thr 5 Leu Val Thr Leu 15 Ser Cys Arg Ser 25 Ser Ser Gly Asn 35 Leu Gln Arg Pro 45 Leu Ile Tyr Leu	(i) SEQUENCE (A) LENG (B) TYPE (C) STRA (D) TOPE (ii) MOLECULE (ix) FEATURE: (A) NAME variable (xi) SEQUENCE Val Val Met Thr Gln 5 Leu Val Thr Leu Gly 15 Ser Cys Arg Ser Ser 25 Ser Ser Gly Asn Thr 35 Leu Gln Arg Pro Gly 45 Leu Ile Tyr Leu Val	(i) SEQUENCE CHARACTERS (A) LENGTH: (B) TYPE: A (C) STRANDER (D) TOPOLOGY (ii) MOLECULE TYPE (ix) FEATURE: (A) NAME/KEY variable reg: (xi) SEQUENCE DESC Val Val Met Thr Gln Ser 5 Leu Val Thr Leu Gly Gln 15 Ser Cys Arg Ser Ser Gln 25 Ser Ser Gly Asn Thr Tyr 35 Leu Gln Arg Pro Gly Gln 45 Leu Ile Tyr Leu Val Ser	(i) SEQUENCE CHARACT (A) LENGTH: 112 (B) TYPE: aming (C) STRANDEDNESS (D) TOPOLOGY: (ii) MOLECULE TYPE: p (ix) FEATURE: (A) NAME/KEY: variable region. (xi) SEQUENCE DESCRIPT Val Val Met Thr Gln Ser Pro 5 Leu Val Thr Leu Gly Gln Pro 15 Ser Cys Arg Ser Ser Gln Ser 25 Ser Ser Gly Asn Thr Tyr Leu 35 Leu Gln Arg Pro Gly Gln Ser 45 Leu Ile Tyr Leu Val Ser Lys	(i) SEQUENCE CHARACTERIST (A) LENGTH: 112 amin (B) TYPE: amino acc (C) STRANDEDNESS: (D) TOPOLOGY: lines (ii) MOLECULE TYPE: polyr (ix) FEATURE: (A) NAME/KEY: Hun variable region. (xi) SEQUENCE DESCRIPTION: Val Val Met Thr Gln Ser Pro Pro 5 Leu Val Thr Leu Gly Gln Pro Ala 15 Ser Cys Arg Ser Ser Gln Ser Leu 25 Ser Ser Gly Asn Thr Tyr Leu Asn 35 Leu Gln Arg Pro Gly Gln Ser Pro 45 Leu Ile Tyr Leu Val Ser Lys Leu	(A) LENGTH: 112 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (ix) FEATURE: (A) NAME/KEY: Humanized variable region. (xi) SEQUENCE DESCRIPTION: SEQ I Val Val Met Thr Gln Ser Pro Pro Ser 5 10 Leu Val Thr Leu Gly Gln Pro Ala Ser 15 20 Ser Cys Arg Ser Ser Gln Ser Leu Leu 25 30 Ser Ser Gly Asn Thr Tyr Leu Asn Trp 35 40 Leu Gln Arg Pro Gly Gln Ser Pro Gln 45 50 Leu Ile Tyr Leu Val Ser Lys Leu Glu	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (ix) FEATURE: (A) NAME/KEY: Humanized LO-CD2a variable region. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88: Val Val Met Thr Gln Ser Pro Pro Ser 5 10 Leu Val Thr Leu Gly Gln Pro Ala Ser 15 20 Ser Cys Arg Ser Ser Gln Ser Leu Leu 25 30 Ser Ser Gly Asn Thr Tyr Leu Asn Trp 35 40 Leu Gln Arg Pro Gly Gln Ser Pro Gln 45 50 Leu Ile Tyr Leu Val Ser Lys Leu Glu	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (ix) FEATURE: (A) NAME/KEY: Humanized LO-CD2a light variable region. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88: Val Val Met Thr Gln Ser Pro Pro Ser 5 10 Leu Val Thr Leu Gly Gln Pro Ala Ser 15 20 Ser Cys Arg Ser Ser Gln Ser Leu Leu 25 30 Ser Ser Gly Asn Thr Tyr Leu Asn Trp 35 40 Leu Gln Arg Pro Gly Gln Ser Pro Gln 45 50 Leu Ile Tyr Leu Val Ser Lys Leu Glu

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile 75 80 Ser Gly Val Glu Ala Glu Asp Val Gly Val 85 90 Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu 105 110

Ile Lys

- INFORMATION FOR SEQ ID NO: 89: (2)
 - (i) SEQUENCE CHARACTERISTICS:
 - LENGTH: 112 amino acids (A)
 - TYPE: amino acid (B)
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (ix) FEATURE:
 - NAME/KEY: Light chain vairable region of (A) HUM5400
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Asp Val Val Met Thr Gln Ser Pro Leu Ser

10

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser

5

۷a:	Leu	Ser	Gln	Ser	Ser	Arg	Cys	Ser	Ile
30					25				
Tr	Asn	Leu	His	Thr	Asn	Gly	Asp	Ser	Tyr
4 (35				
Arg	Pro	Ser	Gln	Gly	Pro	Arg	Gln	Gln	Phe
50					45				
Asp	Arg	Asn	Ser	Val	Lys	Tyr	Ile	Leu	Arg
60					55				
Sei	Gly	Ser	Phe	Arg	Asp	Pro	Val	Gly	Ser
70					65				
Ile	Lys	Leu	Thr	Phe	Asp	Thr	Gly	Ser	Gly
80					75				
Va]	Gly	Val	Asp	Glu	Ala	Glu	Val	Arg	Ser
90					85				
Pro	Trp	His	Thr	Gly	Gln	Met	Cys	Tyr	Tyr
100					95				
Glı	Leu	Lys	Thr	Gly	Gln	Gly	Phe	Thr	Tyr
110					105			•	

(2) INFORMATION FOR SEQ ID NO: 90:

Ile Lys

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 807 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polynucleotide
- (ix) FEATURE:
- (A) NAME/KEY: Nucleotide sequence encoding humanized LO-CD2a light chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AAGCTTCATG	ATGAGTCCTG	TCCAGTCCCT	GTTTCTGTTA	TTGCTTTGGA	TTCTGGGTAA	60
GTAGAGAATG	AGTTACAGGA	CAAGAATGGG	GATGGAGGAT	GAGTTCTGAC	TGCCCATGTT	120
GGCTGTCCAT	GTGTGGTAAG	GCAGGTCCTA	TTTTCTAAGA	TGGACACTTG	AGATTCCATT	180
ACTTGATAAT	GAGAAATTAC	AGATGAGATA	GGATTTGTGC	TAAGAGGATT	CTAATGTAGA	240
TGAGAAGGTG	TATGCCATTT	AGGATCTGCA	ACCGAATTGT	TTTGTGAAAA	AGCATTTGGT	300
ATATTTTTA	AAAATCACAA	AACACACCGG	GATCTCACAG	GAAATGAGTA	ACAAAAAGTA	360
ATTCACAAAG	ATTGGTTGCA	AATTTTGCAC	ATAACTTTGT	TCTGATCTAT	TATAATTTCA	420
GGAACCAATG	GTGATGTTGT	GATGACCCAG	AGTCCACCTT	CATTATTGGT	AACCTTGGGA	480
CAACCAGCTT	CCATCTCTTG	CAGGTCAAGT	CAGAGTCTCT	TACATAGTAG	TGGAAACACC	540
TATTTAAATT	GGTTGCTACA	GAGGCCAGGC	CAATCTCCAC	AGCCGCTAAT	TTATTTGGTA	600
TCCAAACTGG	AATCTGGGGT	CCCCGACAGG	TTCAGTGGCT	CAGGGAGTGG	AACAGATTTC	660
ACACTCAAAA	TCAGTGGAGT	GGAAGCTGAG	GATGTGGGGG	TTTATTACTG	CATGCAATTT	720
ACCCATTATC	CGTACACGTT	TGGACAAGGG	ACCAAGCTGG	AAATCAAACG	TGAGTAGAAT	780
TTAAACTTTG	CTTCCTCAGT	TGGATCC				807

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

(A) NAME/KEY: Humanized LO-CD2a light chain variable region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Met Met Ser Pro Val Gln Ser Leu Phe Leu Leu

-20 -15 -10

Leu Leu Trp Ile Leu Gly Thr Asn Gly Asp

-5 -1 +1

Val Val Met Thr Gln Ser Pro Pro Ser

5

10

Leu Leu Val Thr Leu Gly Gln Pro Ala Ser

15 20

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu

25 30

His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

35 40

Leu Leu Gln Arg Pro Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Val Gly Val

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu

105 110

Ile Lys

- (2) INFORMATION FOR SEQ ID NO: 92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Rat LO-CD2a heavy chain variable region.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu

5

10

Leu Gln Arg Pro Gly Ala Ser Val Lys Leu

15 20

Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr

25 30

Glu Tyr Tyr Met Tyr Trp Val Lys Gln Arg

Pro Lys Gln Gly Leu Glu Leu Val Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 60

Val Glu Lys Phe Lys Lys Lys Ala Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr

75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp

85 90

Thr Ala Thr Tyr Phe Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

105

Gly Thr Leu Val Thr Val Ser Ser

115

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

- (A) NAME/KEY: Humanized LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

5

15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

25 30

Glu Tyr Tyr Met Tyr Trp Val Arg Gln Ala

35 40

Pro Gly Gln Gly Leu Glu Leu Met Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 60

Val Glu Lys Phe Lys Lys Lys Val Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

75 80

Met Glu Leu Ser Ser Leu Thr Ser Asp Asp

85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

Gly Thr Leu Val Thr Val Ser Ser

- (2) INFORMATION FOR SEQ ID NO: 94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Human Amu 5-3 heavy chain variable region.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

5 10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

25 30

Gly Tyr Tyr Met His Trp Val Arg Gln Ala

35 40

Pro Gly Gln Gly Leu Glu Trp Met Gly Arg

Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr

55 60

Ala Gln Lys Phe Gln Gly Arg Val Thr Met

65 . 70

Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr

75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg

95

Thr Glu Tyr Ile Val Val Ala Glu Gly Phe
105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
115 120

Val Ser Ser

- (2) INFORMATION FOR SEQ ID NO: 95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 701 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polynucleotide
 - (ix) FEATURE:

- (A) NAME/KEY: Nucleotide sequence encoding LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

60	CAGGTAAGGC	GCAGTAGCTA	CTTCTTGATG	GGATCATCCT	AAATGCAGGT	AAGCTTCATG
120	TATCTTTGGA	ACAGTGACAC	CACTTGGGAG	AGAGATCATA	CCTAAACTTG	ACTCCCAAGT
180	TGAGGTGAAG	AGTCTGGGGC	CAGCTGGTGC	CTCACAGGTG	CAGGGGTCAA	TTTCTTTCAA
240	CACCGAGTAC	GATACACCTT	AAGGCTTCTG	GGTCTCCTGC	CCTCAGTGAA	AAGCCTGGGG
300	AAGGATCGAT	AGCTGATGGG	CAAGGGCTTG	GGCCCCTGGA	GGGTGCGACA	TATATGTACT
360	CCTGACCGCT	AAAAGGTCAC	AAGTTTAAGA	TTATGTTGAG	GTAGTATTGA	CCTGAAGACG
420	CGACACGGCC	TGACCTCTGA	CTGAGCAGCC	CTACATGGAG	CTAGCACAGC	GACACGTCCT
480	CCAAGGAACC	CTTACTGGGG	TATAGGTTTG	AAAGTTTAAC	GTGCGAGAGG	GTGTATTACT
· 540	GCTTAAATAG	CTTCTATTCA	CAACCTCTCT	TGAGTCCTTA	TCTCCTCAGG	CTGGTCACCG
600	ATGAAGGACT	ATTTCAGGTC	GTGTATCTGA	GGGGAAATGT	ATTTGTTGGG	ATTTTACTGC
660	GACAGACATC	GGCTGATGCA	TGGGAGCCCG	AAAGGGTCAT	TGGGAGTCAG	AGGGACACCT
701	a .	С	TATAGGGATC	GCCAGAGATT	GGACTTCATG	CTCAGCTCCC

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:
 - (A) NAME/KEY: Humanized LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Leu	Phe	ьeu	шe	шe	Trp	Arg	Cys	ьуs	Met
-10					-15				-19
Gln	Ser	Asn	Val	Gly	Thr	Ala	Val	Ala	Met
1	-1				-5				
	Glu	Ala	Gly	Ser	Gln	Val	Leu	Gln	Val
	10					5			
Val	Lys	Val	Ser	Ala	Gly	Pro	Lys	Lys	Val
20					15				
Thr	Phe	Thr	Tyr	Gly	Ser	Ala	Lys	Cys	Ser
30					25				
Ala	Gln	Arg	Val	Trp	Tyr	Met	Tyr	Tyr	Glu
40					35				
Arg	Gly	Met	Leu	Glu	Leu	Gly	Gln	Gly	Pro
50					45				
Tyr	Asp	Ile	Ser	Gly	Asp	Glu	Pro	Asp	Ile
60					55				
Leu	Thr	Val	Lys	Lys	Lys	Phe	Lys	Glu	Val
70					65				
Tyr	Ala	Thr	Ser	Ser	Ser	Thr	Asp	Ala	Thr
80					75				
Asp	Asp	Ser	Thr	Leu	Ser	Ser	Leu	Glu	Met
90					85				
Lys	Gly	Arg	Ala	Cys	Tyr	Tyr	Val	Ala	Thr
100					95				
Gln	Gly	Trp	Tyr	Ala	Phe	Arg	Tyr	Asn	Phe

Gly Thr Leu Val Thr Val Ser Ser